

[illegible][illegible]

[illegible][illegible][illegible][illegible]

FIG. 4

CAATCATTTTGGATCACTGGACTTTTCAGTGGACTACCTAAACAGGGGACAGCTTTTGGA
AGATGACATCTGCAATGCTTTTCATCTTTACCAACGGCAAGCCTTTCTGCACAGAGAGCA
CAGCAGAATGGCTCCTGTCACTGCATTCCAATGGCAGCTGTACTATCTACCAACCGTGCT
GAGGACAGCACCAAAGGTTCTCTCCTCACCCACATGCCTGAAAAGCACATGTGAATTC
GTGTATAGTGGGCTGAGGTGCAGCTGATCTCTAGCTAATCAACACAACCCACCAACAAAT
GACCACAGGTGGCACTGTGTGGTCTTTACATCGGGTTGCACTGTCCATGAAATAGAAA
CACTCACAAACATCTGATTCCAGTGTGGCCATAATAACAGAAATCTAACAACCTCTTTCCTT
GCCTTTTCAATATCAAATAAAACCATCAGCATCCTGCTGGATTGATAGCAAAGGATTTCC
AAAAATATTCATCTACCCGAAGTCCTCCTCTGTGAAGGCCGGTGGAGTAGCCACTTTGAAA
ACAGAACTTCCAACCAGGTTACCATGTCTAACCTATGACCAGAGAGTCACACTGATGAAG
CCTCATACCATTTGCCTTTTGGATTTTATTTAATATCAGAAGAGATGAATTCTTAAGATA
TTTTTCTGAAGGTTGCCCAGGGCACAAACAAATTGGACACTTTCACTGCTAAAAAGTACA
CTTTAATATTCTTAAAGTATAATTTCTTTAGAGCAGTATCCCTAT'TGCTGGCAAGTTCTG
CTTTCATAAAATATGCAGATAAGAAGTGTTAAATGGGATTCAAGAATTATGGTTTTTATTT
GGGACTGTTTGCATACTCACAATGGTTTTGTTCTCATTGTTTTTAACAAAAAAGCAATGA
AGTTTGGGGTGGTTTTTTGAAAACGAACTGAAAAAAATTATATGTGAAAATGAGAACTG
GGTAAATAAAATTATATTTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAG

FIG. 5

ATGTTCTTTCTACTTCATTTTCATCGTTCTGATCAATGTCAAAGATTTTGCACTGACTCAA
GGTAGCATGATCACTCCTTCATGCCAAAAAGGATATTTTCCCTGTGGGAATCTTACCAAG
TGCTTACCCCGAGCTTTTCTACTGTGATGGCAAGGATGACTGTGGGAACGGGGCGGACGAA
GAGAACTGTGGTGACACTAGTGGATGGGCGACCATATTTGGCACAGTGCAATGGAAATGCT
AACAGCGTGGCCTTAACACAGGAGTGCTTTCTAAAACAGTATCCACAATGCTGTGACTGC
AAAGAACTGAATTGGAATGTGTAAATGGTGACTTAAAGTCTGTGCCGATGATTTCTAAC
AATGTGACATTACTGTCTCTTAAGAAAAACAAAATCCACAGTCTTCCAGATAAAGTTTTT
ATCAAATACACAAAACCTTAAAAAGATATTTCTTCAGCATAATTGCATTAGACACATATCC
AGGAAAAGCATTTTTTTGGATTATGTAATCTGCAAATATTAATTCTAGATGACAATCCAATA
ACCAGAATTTACAGCGCTTGTTTTACGGGATTAAATTCCTTGTTTTTCTGTCTATGGTT
AATAACTACTTAGAAGCTCTTCCCAAGCAGATGTGTGCCCAAATGCCTCAACTCAACTGG
GTGGATTTGGAAGGCAATAGAATAAAGTATCTCACAATTTCTACGTTTTCTGTCTGCGAT
TCGCTCACAGTGCTGTTTTCTGCCTAGAAATCAAATTTGGTTTTGTTCCAGAGAAGACATTT
TCTTCATTAATAAATTTAGGAGAACTGGATCTGTCTAGCAATACGATAACGGAGCTATCA
CCTCACCTTTTTAAAGACTTGAAGCTTCTACAAAAGCTGAACCTGTCAATCCAATCCTCTT
ATGTATCTTCAACAAGAACCAGTTTGAAAGTCTTAAACAACCTTCAGTCTCTAGACCTGGAA
AGGATAGAGATTCCAAATATAAACACACGAATGTTTTCAACCCATGAAGAATCTTCTCAC
ATTTATTTCAAAAACCTTCGATACTGCTCCTATGCTCCCCATGTCCGAATATGTATGCCC
TTGACGGACGGCATTCTTCATTTGAGGACCTCTTGGCTAACAATATCCTCAGAATATTT
GTCTGGGTTATAGCTTTCATTACCTGCTTTGGAAATCTTTTTGTCAATTGGCATGAGATCT
TTCATTAAAGCTGAAAATACAACCTCACGCTATGTCCATCAAATCCTTTGTTGTGCTGAT
TGCTTGATGGGTGTTTTACTTGTTCTTTGTTGGCATTTCGATATAAAATACCGAGGGCAG
TATCAGAAGTATGCCTTGCTGTGGATGGAGAGCGTGCAGTGCCGCCTCATGGGGTTCCCTG
GCCATGCTGTCCACCGAAGTCTCTGTTCTGCTACTGACCTACTTGACTTTGGAGAAGTTC
CTGGTCATTGTCTTCCCCTTCAGTAACATTGACCTGGAAAACGGCAGACCTCAGTCATC
CTCATTGTCATCTGGATGGCGGGATTTTTAATAGCTGTAATTCATTTTGGGAATAAGGAT
TATTTTGGAACTTTTATGGGAAAAATGGAGTATGTTTCCCACTTTATTATGACCAAACA
GAAGATATTGGAAGCAAAGGGTATTCTCTTGGAATTTTCTAGGTGTGAACCTGCTGGCT
TTTCTCATCATTGTGTTTTCTATATTACTATGTTCTGTTCCATTCAAAAACCGCCTTG
CAGACCACAGAAGTAAGGAATTGTTTTGGAAGAGAGGTGGCTGTTGCAAATCGTTTCTTT
TTTATAGTGTTCTCTGATGCCATCTGCTGGATTCTGTATTTGTAGTTAAAATCCTTTCC
CTCTTCCGGGTGGAAATACCAGACACAATGACTTCTTGATAGTGATTTTTTTCTTCCA
GTTAACAGTGCTTTGAATCCAATCCTCTATACTCTCACAACCACTTTTTTTAAGGACAAG
TTGAAACAGCTGCTGCACAAACATCAGAGGAAATCAATTTTCAAATTAATAAAAAAAGT
TTATCTACATCCATTGTGTGGATAGAGGACTCCTCTTCCCTGAAACTTGGGGTTTTGAAC
AAAATAACACTTGAGACAGTATAATGAAACCAGTTTCCTAG

FIG. 6

MFFLLHFIVLINVKDFALTQGSMTIPSCQKGYFPCGNLTKCLPRAFHCDGKDDCGNGADE
 ENCGDTSGWATIFGTVHGNANSVALTQECFLKQYPQCCDCKETELEC VNGDLKSVP MISN
 NVTLLSLKKNKIHS L PDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILILDDNPI
 TRISQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLNWVDLEGNRIKYL TNSTFLSCD
 SLTVLFLPRNQIGFVPEKTFSS LKNLGELDLSSNTITELSPHLFKDLKLLQKLNLSNPL
 MYLHKNQFESLQQLQSLDLERIEIPNINTRMFQPMKNLSHIYFKNFRYCSYAPHVRICMP
 LTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRSFIKAENTTHAMSIKILCCAD
 CLMGVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVS VLLLTYLTLEKF
 LVIVFPFSNIRPGKRQTSVILICIWMAGFLIAVIPFWNKDYFGNFYGKNGVCFPPLYDQT
 EDIGSKGYSLGIFLGVNLLAFLIIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFF
 FIVFSDAICWIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDK
 LKQLLHKHQKRSIFKIKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPVS

FIG. 7

MFFLLHFIVL INVKDFALTQ GSMITPSCQK GYFPCGNLTK CLPRAFHCDG
 KDDCGNGADE ENCGDTSGWA TIFGTVHGNA NSVALTQECF LKQYPQCCDC
 KETELEC VNG DLKSVP MISN NVTLLSLKKN KIHS L PDKVFIKYTKLKKIF
 LQHNCIRHIS RKAFFGLCNL QILYLNHN CI TTLRPGIFKD LHQLTWLILD
 DNPITRISQR LFTGLNSLFF LSMVNNYLEA LPQMCAQMP QLNWVDLEGN
 RIKYL TNSTF LSCDSLTVLF LPRNQIGFVP EKTFFSS LKNL GELDLSSNTI
 TELSPHLFKD LKLLQKLNLS SNPLMYLHKN QFESLQQLQS LDLERIEIPN
 INTRMFQPMK NLSHIYFKNF RYCSYAPHVR ICMPLTDGIS SFEDLLANNI
LRIFVWVIAF ITCFGNLFVI GMRSF IKAE N TTHAMSIKIL CCADCLMGVY
LFFVGIFDIK YRGQYQKYAL LWMESVQCRL MGFLAMLSTE VSVLLLTYLT
LEKFLVIVFP FSNIRPGKRQ TSVILICIWM AGFLIAVIPF WNKDYFGNFY
 GKNGVCFP LY YDQTEDIGSK GYSLGIFLGV NLLAFLIIIVF SYITMFCSIQ
 KTALQTTEVR NCFGREVAVA NRFFFIVFSD AICWIPVFV V KILSLFRVEI
 PDTMTSWIVI FFLPVNSALN PILYTLTTNF FKDKLQLLH KHQKRSIFKI
 KKKSLSTSIV WIEDSSSLKL GVLNKITLGD SIMKPVS

FIG. 8A

```
HGPRBMY5 ~~~~~
HGPRBMY5_splice ~~~~~
GPCR_LYMST MATMSGTTIVCLIIYLTMTLGN SQGVNLKIESPSPPTLCSVEGTFHCDDGM
FSHR_RAT ~~~~~
Q64183 ~~~~~
FSHR_EQUAS ~~~~~
FSHR_CHICK ~~~~~
LSHR_CALJA ~~~~~
O75473 ~~~~~

HGPRBMY5 ~~~~~
HGPRBMY5_splice ~~~~~
GPCR_LYMST LQCVLMGSKCDGVSDCENGMDSESVETCGCLQSEFQCNHTTCIDKILRCDR
FSHR_RAT ~~~~~
Q64183 ~~~~~
FSHR_EQUAS ~~~~~
FSHR_CHICK ~~~~~
LSHR_CALJA ~~~~~
O75473 ~~~~~

HGPRBMY5 ~~~~~
HGPRBMY5_splice ~~~~~
GPCR_LYMST NDDCSNGLDERECDIYICPLGTHVKWHNHFCVPRDKQCDFLDDCGDNSDE
FSHR_RAT ~~~~~
Q64183 ~~~~~
FSHR_EQUAS ~~~~~
FSHR_CHICK ~~~~~
LSHR_CALJA ~~~~~
O75473 ~~~~~

HGPRBMY5 ~~~~~
HGPRBMY5_splice ~~~~~
GPCR_LYMST KICERRECVATEFKCNNSQCVAFGNLC DGLVDCVDGSDDEDQVACDS DKYF
FSHR_RAT ~~~~~
Q64183 ~~~~~
FSHR_EQUAS ~~~~~
FSHR_CHICK ~~~~~
LSHR_CALJA ~~~~~
O75473 ~~~~~

HGPRBMY5 ~~~~~
HGPRBMY5_splice ~~~~~
GPCR_LYMST QCAEGSLIKKEFVCDGWVDCKLTFAD ELNCKLCDEDDFRCS DTRCIQKSN
FSHR_RAT ~~~~~
Q64183 ~~~~~
FSHR_EQUAS ~~~~~
FSHR_CHICK ~~~~~
LSHR_CALJA ~~~~~
O75473 ~~~~~~MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRG

HGPRBMY5 ~~~~~
HGPRBMY5_splice ~~~~~
GPCR_LYMST VCDGYCDCKTCDD EVCANNTYGC PMDTKYMCRSIYGEPRCIDKDNVCNM
```

FIG. 8B

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FSHR_RAT      ~~~~~
Q64183        ~~~~~
FSHR_EQUAS    ~~~~~
FSHR_CHICK    ~~~~~
LSHR_CALJA    ~~~~~
O75473        CPTHCHCEPDGRMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLLP

HGPRBMY5      ~~~~~~MFFLLHF
HGPRBMY5_splice ~~~~~~MFFLLHF
GPCR_LYMST    INDCRDGNVGTDEYYCSNDSECKNFQAAMGFFYCPEERCLAKHLYCDLH.
FSHR_RAT      ~~~~~
Q64183        ~~~~~
FSHR_EQUAS    ~~~~~
FSHR_CHICK    ~~~~~
LSHR_CALJA    ~~~~~
O75473        NPLPSLRFLLEELRLAGNALTYPKGAFTGLYSLKVLMLQNNQLRHVPTEA

HGPRBMY5      IVLINVKDFALTQGSMTTPSCQKGYFPCGNLTCKLPRAFHC DGKDDCGNG
HGPRBMY5_splice IVLINVKDFALTQGSMTTPSCQKGYFPCGNLTCKLPRAFHC DGKDDCGNG
GPCR_LYMST    PDCINGED...EQSCLAPPKCSQDEFQCHH.GKCIPISKRCDSVHDCVDW
FSHR_RAT      ~~~~~
Q64183        ~~~~~
FSHR_EQUAS    ~~~~~
FSHR_CHICK    ~~~~~
LSHR_CALJA    ~~~~~
O75473        LQNLRLSLQSLRLDANHISYVPPSCFSGLHSLRHLWLDDNALTEIPVQAFR

HGPRBMY5      ADEENCGDTSGWATIFGTVHGNANSVALTQEC.FLKQYP....QCCD..
HGPRBMY5_splice ADEENCGDTSGWATIFGTVHGNANSVALTQEC.FLKQYP....QCCD..
GPCR_LYMST    SDEMNCENHQCAANMKSCSLSGHC..IEEHKWCNHFHRECPDGSDEKDCDPR
FSHR_RAT      ~~~~~~MALLLVSL...AFLGTGSGCHHWL
Q64183        ~~~~~~MALLLVSL...AFLGTGSGCHHWL
FSHR_EQUAS    ~~~~~~MALLLVSL...AFLSLGSGCHHQV
FSHR_CHICK    ~~~~~~MSLGLTCL...ILLASCSCQHHT
LSHR_CALJA    ~~~~~~MKQPLLALQLLKL...PLPPLPRALREAR
O75473        SLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSLGKKCFDGL

HGPRBMY5      ..CKETELEC VNG...DLKSVPMISNNVTLLSLKKNKT...HSLPD...
HGPRBMY5_splice ..CKETELEC VNG...DLKSVPMISNNVTLLSLKKNKT...HSLPD...
GPCR_LYMST    PVCEANQFRCKNGQCIDPLQVCVKGDYDGCADQSHLINCSQHICLEGQF
FSHR_RAT      CHCSNRVFLCQDSKVTEIPDLPR..NAIELRFVLTCLRVIKGSFAGFG
Q64183        CHCSNRVFLCQDSKVTEIPDLPR..NAIELRFVLTCLRVIKGSFAGFG
FSHR_EQUAS    CHYSNRVFLCQESKVTEIPSDLPR..NAELRFVLTCLRVIKGAFGSGFG
FSHR_CHICK    CLCEGRIFHCQEIKVQLPRDIPT..NATELRFVLTCLRVIKGAFTGLH
LSHR_CALJA    C.CPEPC.NCTPDGALRCPGP.GA..GLTRLSLAYLPVKVIPSQAFRGLN
O75473        .HSLETLEL.NYNNLDEFFPAARTLSNLKELGFHSNNIRSIPEKAFVGNP

HGPRBMY5      ...KVF.IKYTK.....LKKIFLQH.NCIRHISRKAFFGL
HGPRBMY5_splice ...KVF.IKYTK.....LKKIFLQH.NCIRHISRKAFFGL
GPCR_LYMST    RCRKSFICINQTKVCD.....GTVDCLQGMWDEN.NC.RYWCPHG.QAI
Q64183        DLEKI.EISQNDVLEVIADVFSNLPKLHEIRIEKANNLLYINPEAFQNL
FSHR_RAT      DLEKI.EISQNDVLEVIADVFSNLPKLHEIRIEKANNLLYINPEAFQNL
FSHR_EQUAS    DLKKI.EISQNDVLEVIADVFSNLPKLHEIRIEKANNLLYIDHDAFQNL

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FIG. 8C

FSHR_CHICK DLEKI.EISONDALIEIIEGNVFSSLPKLHEIRIEKANKLMKIDQDAFOHL
 LSHR_CALJA EVIKI.EISQSDSLERIEANAFDNLNLSEILITQNTKNLTHIEPGAFTNL
 075473 SLITI.HFYDNP.IQFVGRSAFOHLPELRTITLNGASOITEF.PD.LTGT

HGPRBMY5 CNLQIILYNHNCITTLRPGIFKDLHQL.TWLILD..DN.PITRISQRLF.
 HGPRBMY5_splice CNLQI.....LILD..DN.PITRISQRLF.
 GPCR_LYMST COCEGVMTDCTGOKLKEMPVQOMEEDL.SKLMIG..DN..LLNTTSTTFS
 FSHR_RAT PSLRYLLISNTGIKHL..AVHKIQSLQ.KVLLDIQDNINHIIVARNSEFM
 Q64183 PSLRYLLISNTGIKHL..AVHKIQSLQ.KVLLDIQDNINHIIVARNSEFM
 FSHR_EQUAS PNLOYLLISNTGIKHL..AVHKIQSLQ.KVLLDIQDNINHIIVARNSEFM
 FSHR_CHICK PSLRYLLISNTGLSFLP..VVHKVHSFQ.KVLLDVQDNTHIRTIERNTEFM
 LSHR_CALJA BRLLKYLSTCNTGIRKFP..DVTKIFSSETNFILICDNLHITTPGNAFO
 075473 ANLESLLTGAQISSLPQTVCNQLPNLQ...VLDSLYNL.IEDLP..SF.

HGPRBMY5 .TGLNSLFFLSMVNNYIEALPKQMCAQMPQLNWDLEGN.RIKYLTNSTF
 HGPRBMY5_splice .TGLNSLFFLSMVNNYIEALPKQMCAQMPQLNWDLEGN.RIKYLTNSTF
 GPCR_LYMST ATYYDKVTYLDLSRNHLTEIPIYSFQNMWKLTHLNLADN.NITSLKNGSL
 FSHR_RAT GLSFESVI.LWLSKNGIEEIHNCFAFNG.TQDELNLSDNNNLEELPNDVF
 Q64183 GLSFE....WLSKNGIEEIHNCFAFNG.TQDELNLSDNNNLEELPNDVF
 FSHR_EQUAS GLSFESMI.LRLSKNGIQEIHNCFAFNG.TQDELNLSDNNNLEELPNDVF
 FSHR_CHICK GLSSESVI.LRLNKGIEEIKDHAFNG.TCLDELNLSDYNLEKLPEKVF
 LSHR_CALJA GMMNESIT.LKLYGNGFEEVQSHAFNG.ITTVISLVLKENVHLERTHNGAF
 075473 SVCQKLQK.IDLRHNEIYEIKVDTFQQLLSLRSNLAWN.KIALIHPNAF

HGPRBMY5 LSCDSLTVLFLPRNQIGFVPEKTFSSSLKNLGELDLSSNTITELSPHLFKD
 HGPRBMY5_splice LSCDSLTVLFLPRNQIGFVPEKTFSSSLKNLGELDLSSNTITELSPHLFKD
 GPCR_LYMST LCLSNLKQLHINGNKIETFEEDTFSSMIHLTVLDSLNRQLTHVYKNMFKG
 FSHR_RAT QGASGPVILDISRTKVHSLPNHGLENLKKLRA..RSTYRLKKL.PNLDKF
 Q64183 QGASGPVILDISRTKVHSLPNHGLENLKKLRA..RSTYRWKKL.PNLDKF
 FSHR_EQUAS QGASGPVILDISGTRIHSPLPNYGLENLKKLRA..RSTYNLKKL.PSLEKF
 FSHR_CHICK QGATGPVILDISRTIRISFLPSHGLEFTIKKLR..RSTYKLKKL.PDVNKF
 LSHR_CALJA RGATGPSILDISSTKIQALPSHGLESITQTLIA..TSSYSLKKL.PSREKF
 075473 STLPSLILKLDLSSNLSSFFITGLHGLTHLKL..TGNHALQSL.ISSNF

HGPRBMY5 LKLLQ.KLNLSSNPLMYLH.KNOFESLKQLQSLDLERIEIPNINTRMFQP
 HGPRBMY5_splice LKLLQ.KLNLSSNPLMYLH.KNOFESLKQLQSLDLERIEIPNINTRMFQP
 GPCR_LYMST LKQIT.VLNISRNOINSID.NGAFNNLANVRLIDLSGNVIKDIGQKVMFG
 FSHR_RAT VILMEASLTYP SHCCAFANLKRQISELHPTCNKSILRODIDDMTQIGDQR
 Q64183 VILMEASLTYP SHCCAFANLKRQISELHPTCNKSILRODIDDMTQIGDQR
 FSHR_EQUAS VALMEASLTYP SHCCAFANWRQOTSELQTTCNKSILRQEV.DMTQARGER
 FSHR_CHICK RSLTEANFTYP SHCCAFANRKTQNTFYPICSMSPAKQDLGEQTGKRKRH
 LSHR_CALJA ANLIDATLTYP SHCCAFANRNVPTK.....
 075473 PELKVIEMPVAYQCAF.GVCENAYKISNQWNKGD.NSSMDDL.HKKDAG

HGPRBMY5 MKNL.....SHLYFKNFRY.CSYAPHVRI CMPLTDGISSFEDLLA
 HGPRBMY5_splice MKNL.....SHLYFKNFRY.CSYAPHVRI CMPLTDGISSFEDLLA
 GPCR_LYMST LPRL.....VELKTDSYRF.CCLAPEGVKCSPKQDEFSSCEDLMS
 FSHR_RAT VSLIDDEPS.YGKGSDDMYNEFDYDLCEVVDVTCSPKPDFAFNPCEDIMG
 Q64183 VSLIDDEPS.YGKGSDDMYNEFDYDLCEVVDVTCSPKPDFAFNPCEDIMG
 FSHR_EQUAS VSLAEDDES.....MMYSEFDYDLCEVVDVTCSPKPDFAFNPCEDIMG
 FSHR_CHICK RSAAEDYISHYGTRFGPVNEFDYGLCEVVDVFCSPKPDFAFNPCEDIMG
 LSHR_CALJADYPAIFAESGQSGW.DYDYG.F.HLPKTPRCAPEPDAFNPCEDIMG
 075473 MFQAQDE.....RDLEDFLLDFFEDL.KALHSVQCSPPGPFKPCHEHLD

Fig. 8D

HGPRBMY5 NNILRIFVWVIAFTTCFGNLFVIGMRSFIKAENTHAMS TKILCCADCLM
 HGPRBMY5_splice NNILRIFVWVIAFTTCFGNLFVIGMRSFIKAENTHAMS TKILCCADCLM
 GPCR_LYMST NHVLRVSIWVLGVIALVGNFVLFWRVRDFRGGKVHSFLITNLAIGDFLM
 FSHR_RAT YNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFRFLMCNLAFAADLCI
 Q64183 YNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPFRFLMCNLAFAADLCI
 FSHR_EQUAS YDILRVLIWFISILAITGNIIVLVLTTSQYKLTVPFRFLMCNLAFAADLCI
 FSHR_CHICK YNVLRVLIWFINILAITGNTTVLITLISQYKLTVPFRFLMCNLAFAADLCI
 LSHR_CALJA YDFLRVLIWLINILAIMGNMTVLFVLTTSRYKLTVPFRFLMCNLSFADFCLM
 O75473 GWLLRIGVWTTIAVLALTCLNALVTSTVFRSPLYTSPIKLLIGVTAAVNMLT

HGPRBMY5 GVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLLT
 HGPRBMY5_splice GVYLFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLLT
 GPCR_LYMST GVYLLTIAATADTYRGVYISHDENWKQSGLCQFAGFVSTFSSLSVLTLS
 FSHR_RAT GIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASLSVYTLT
 Q64183 GIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASLSVYTLT
 FSHR_EQUAS GIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASLSVYTLT
 FSHR_CHICK GIYLLFIASVDIHTKSRYHNYAIDWQTGAGCNAAGFFTVFASLSVYTLT
 LSHR_CALJA GLYLLLIASVDSQTKGOYHNYAIDWQTGSGCNTAGFFTVFASLSVYTLT
 O75473 GVSSAVLAGVDAFTFGSFAHGAWENGVGCHVIGELSTFASLSVVELLT

HGPRBMY5 YLTLEKFLVIVFPFS.NIRPGKRQTSVILICIWMAFLIAVTPFWNKDYF
 HGPRBMY5_splice YLTLEKFLVIVFPFS.NIRPGKRQTSVILICIWMAFLIAVTPFWNKDYF
 GPCR_LYMST TITLDRLICILFPLR.RTRIGLROAITVMSCIWVLVELLAVLPPLGFSYF
 FSHR_RAT AITLERWHTITHAMOLECKVOLRHAASVMVLGWTFAFAAALFPFEGISS.
 Q64183 AITLERWHTITHAMOLECKVOLRHAASVMVLGWTFAFAAALFPFEGISS.
 FSHR_EQUAS AITLERWHTITHAMOLECKVOLRHAASVMVLGWTFPGFVGLLPFEGIST.
 FSHR_CHICK VITLERWHTITHAMOLNRKVRRLRHAVTIMVFGWMPAFTVALLPFGISS.
 LSHR_CALJA VITLERWHTITHATHLDOKLRLRHAILIMLGWLFSSSLIAMPPLVGVSN.
 O75473 LAALERGFSSVKYSAKFETKAPFSSSLKVIITLICALTMAAVPLLGSK.

HGPRBMY5 GNFYCKNGVCFPLYDQTEDIGSKGYSLGIFLGVNLLAFLTIIVFSYITMF
 HGPRBMY5_splice GNFYCKNGVCFPLYDQTEDIGSKGYSLGIFLGVNLLAFLTIIVFSYITMF
 GPCR_LYMST ENFYGRSGVCLALHVTDPDRPGWE.VSVGVFTLLNLSEVLIASSYLWME
 FSHR_RAT ...YMKVSICLPMDDISPL...SOLYVMALLV.LNVLAFVVICGCYTHIY
 Q64183 ...YMKVSICLPMDDISPL...SOLYVMALLV.LNVLAFVVICGCYTHIY
 FSHR_EQUAS ...YMKVSICLPMDDISPL...SOLYVMSLLV.LNVLAFVVICGCYTHIY
 FSHR_CHICK ...YMKVSICLPMHETPF...SQAYVIFLLV.LNVLAFVVICICYICIY
 LSHR_CALJA ...YMKVSICFPMDEVETL...SQIVITITLL.LNVVAFIICACYIKIY
 O75473 ...YGASPECLPFPGEPS...TMCYVVALLL.LNSLCFLMMTIAYTKLY

HGPRBMY5 CSIQKT..ALOTTEVRNCFGREVAVANRFFFIVFSDAICWIPVVFVKILS
 HGPRBMY5_splice CSIQKT..ALOTTEVRNCFGREVAVANRFFFIVFSDAICWIPVVFVKILS
 GPCR_LYMST SVAKKTRSAVRTAESKN....DNAMARRMILLVMTDFCCWVPIIVLGFVS
 FSHR_RAT LTVRNPTIVSSSSDTK.....IAKRMATLIFTDFLCMAPISFFAISA
 Q64183 LTVRNPTIVSSSSDTK.....IAKRMATLIFTDFLCMAPISFFAISA
 FSHR_EQUAS LTVRNPNISSSSDTK.....IAKRMATLIFTDFLCMAPISFFAISA
 FSHR_CHICK FTVRNPNISSNSDTK.....IAKRMATLIFTDFLCMAPISFFAISA
 LSHR_CALJA FAVRNPELMATNKDTK.....IAKRMATLIFTDFLCMAPISFFAISA
 O75473 CNLDKGDLENIWDCS.....MVKHTALLIFTNCLNCPVAFLSFSS

FIG. 8E

HGPRBMY5	LFRVE.IPDITMTSWIVIFFLPVNSALNPILYTLTINFFKDKLKQLLHKHQ
HGPRBMY5_splice	LFRVE.IPDITMTSWIVIFFLPVNSALNPILYTLTINFFKDKLKQLLHKHQ
GPCR_LYMST	LAGAR.ADDQVYAWIAVFVLPINSATNPVITYLSTAPFLGNVRKRANRFR
FSHR_RAT	SLKVPLITVSKAKILLVLFYPINSCANPFLYAIFTKNFRRDFFILLSKFG
Q64183	SLKVPLITVSKAKILLVLFYPINSCANPFLYAIFTKNFRRDFFILLSKFG
FSHR_EQUAS	SLKVALITVSKSKILLVLFYPINSCANPFLYAIFTKNFRRDFFILLSKFG
FSHR_CHICK	SLRVPLITVSKSKILLVLFYPINSCANPFLYAIFTKTFRRDFFILLSKFG
LSHR_CALJA	AFKMPLITVTNSKVLLVLFYPINSCANPFLYAIFTKTFRRDFFILLGKFG
O75473	LENLTFISPEVIKFIILLVVVPLPACLNPPLYILFNPHFKED.LVSLRK..
HGPRBMY5	RKSTFKI...KKKSL...STSIVWIEDSSSLKLGVLNKI.TLGDS.IMKP
HGPRBMY5_splice	RKSTFKI...KKKSL...STSIVWIEDSSSLKLGVLNKI.TLGDS.IMKP
GPCR_LYMST	KSFTHSFTGDTKHSYVDDGITHSYCEKKSPYRQLELKRLRSLNSS...PP
FSHR_RAT	CYEMOAOITY.RTETSS..ATHNFHARKSHCSSAPR....VTN..SYVLVP
Q64183	CYEMOAOITY.RTETSS..ATHNFHARKSHCSSAPR....VTN..SYVLVP
FSHR_EQUAS	CYEMOAOITY.RTETSS..TGHISHPKNGPCPPTPR....VTNGANCTLVP
FSHR_CHICK	CCEMOAOITY.RTETSS..SAHNFHTRNGHYPTASK....NSDGTIYSLVP
LSHR_CALJA	CCKHRAEILY.RRKDFS..A.YTSNYKNG.FTGSSK....PSQST..LKLP
O75473QTYVWTRSKHPSLMSINSDDVEKQSCDSTQALVTFTSSSIYDLPP
HGPRBMY5	VS-----
HGPRBMY5_splice	VS-----
GPCR_LYMST	MYNTELSHSDS-----
FSHR_RAT	LNHSSQN-----
Q64183	LNHSSQN-----
FSHR_EQUAS	LSHLAQN-----
FSHR_CHICK	LNHLN-----
LSHR_CALJA	ALHCQGTALLDKTCYKEY-----
O75473	SSVPSPAYPVTESCHLSSVAFVPCL

FIG. 9A

1	MFFLLHFIVLINVKDFALTQGSIMITPSCQKGYFPCGNLT	KCLPRAFHCDG	50		
1	MFFLLHFIVLINVKDFALTQGSIMITPSCQKGYFPCGNLT	KCLPRAFHCDG	50		
51	KDDCGNGADEENCGDTSGWATIFGTVHGNANSVALTQECFLKQYPQCCDC		100		
51	KDDCGNGADEENCGDTSGWATIFGTVHGNANSVALTQECFLKQYPQCCDC		100		
101	KETELEC	VNGDLKSVP	MISNNVTLLSLKKNKIHS	LPDKVFIKYTKLKKIF	150
101	KETELEC	VNGDLKSVP	MISNNVTLLSLKKNKIHS	LPDKVFIKYTKLKKIF	150
151	LQHNCIRHISRK	KAFFGLCNLQILYLNHNCITTLRPGIFKDLHQLTWLILD		200	
151	LQHNCIRHISRK	KAFFGLCNLQI.....LILD		176	
201	DNPITRISQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLN	NWVDLEGN	250		
177	DNPITRISQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLN	NWVDLEGN	226		
251	RIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTI		300		
227	RIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKTFSSLKNLGELDLSSNTI		276		
301	TELSPHL	FKDLKLLQKLNLSNPLMYLHKNQFESLKQLQSLDLERIEIPN	350		
277	TELSPHL	FKDLKLLQKLNLSNPLMYLHKNQFESLKQLQSLDLERIEIPN	326		
351	INTRMFQPMKNLSHIYFKNFRYCSYAPHV	RICMPLTDGISSFEDLLANNI	400		
327	INTRMFQPMKNLSHIYFKNFRYCSYAPHV	RICMPLTDGISSFEDLLANNI	376		
401	LRIFVWVIAFITCFGNL	LVIGMRSFIKAENTTHAMSIKILCCADCLMGVY	450		
377	LRIFVWVIAFITCFGNL	LVIGMRSFIKAENTTHAMSIKILCCADCLMGVY	426		
451	LFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVS	VLLLLTYLT	500		
427	LFFVGIFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVS	VLLLLTYLT	476		
501	LEKFLVIVFPFSNIRPGKRQTSVILICIWMAGFLIAV	IPFWNKDYFGNFY	550		
477	LEKFLVIVFPFSNIRPGKRQTSVILICIWMAGFLIAV	IPFWNKDYFGNFY	526		
551	GKNGVCFPLYDQTEDIGSKGYSLGIFLGVNLLAFLII	VFSYITMFCSIQ	600		
527	GKNGVCFPLYDQTEDIGSKGYSLGIFLGVNLLAFLII	VFSYITMFCSIQ	576		

FIG. 9B

601 KTALQTTEVRNCFGREVAVANRFFFIVFSDAICWIPVFVVKILSLFRVEI 650
|||||
577 KTALQTTEVRNCFGREVAVANRFFFIVFSDAICWIPVFVVKILSLFRVEI 626

651 PDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDKLKQLLHKHQKSIFKI 700
|||||
627 PDTMTSWIVIFFLPVNSALNPILYTLTTNFFKDKLKQLLHKHQKSIFKI 676

701 KKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPVS 737
|||||
677 KKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIMKPVS 713

102250" 3663660

FIG. 10

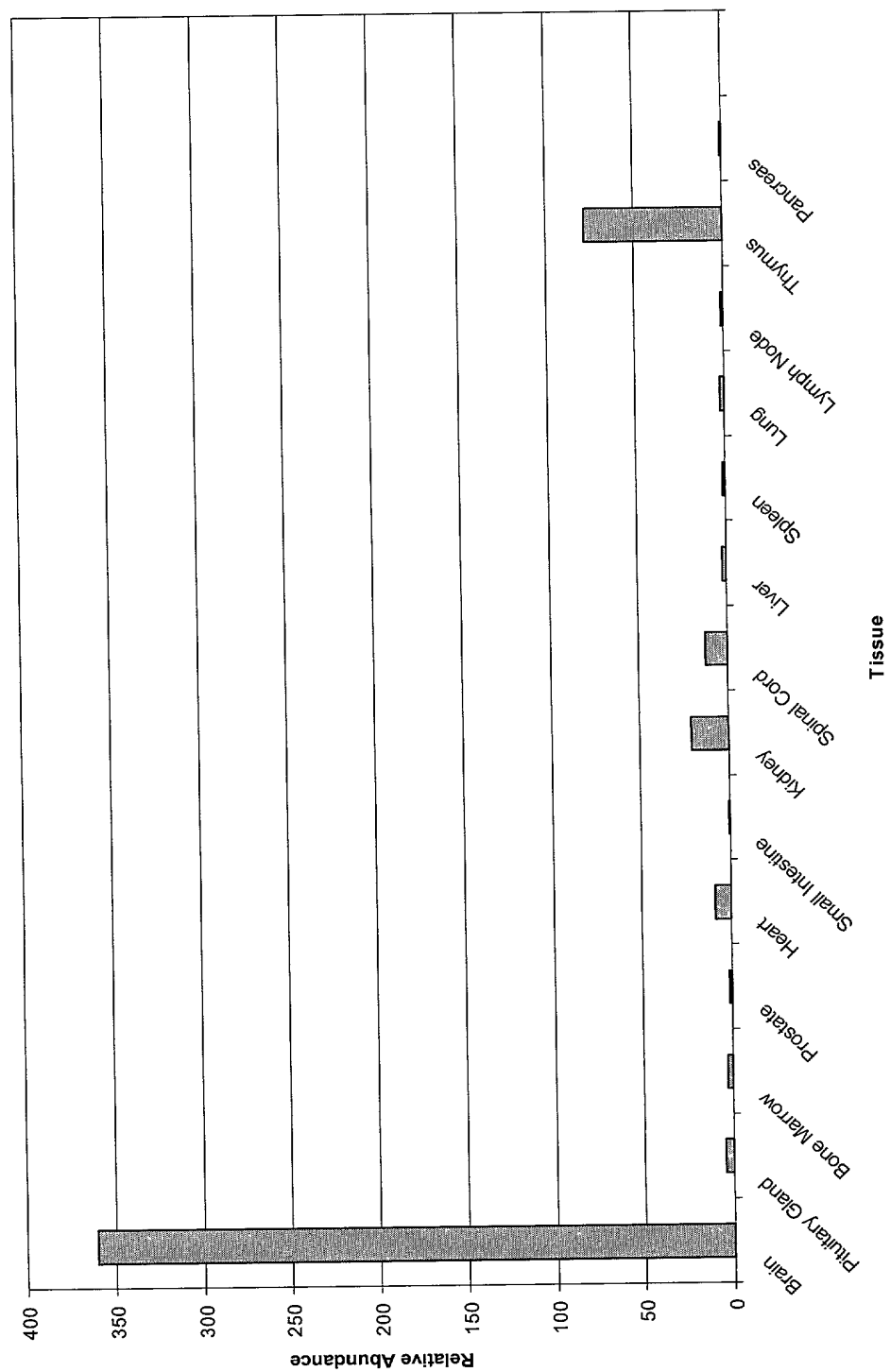


FIG. 11

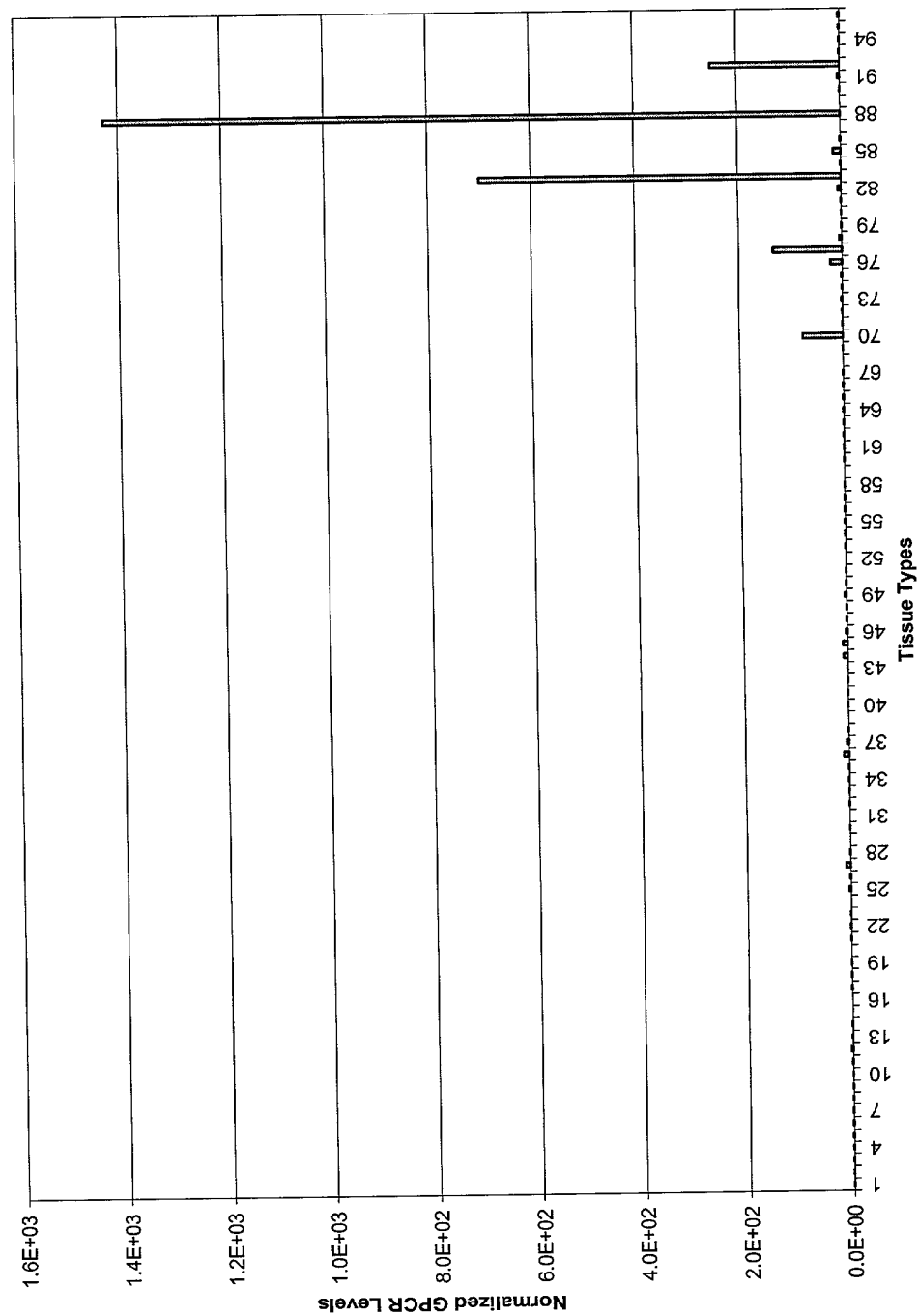


FIG. 12

